
Reversible Regulation of Promoter and Enhancer Histone Landscape by DNA Methylation in Mouse Embryonic Stem Cells.

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Public Summary:

DNA methylation is one of a number of modes of epigenetic gene regulation. Here, we profile the DNA methylome, transcriptome, and global occupancy of histone modifications (H3K4me1, H3K4me3, H3K27me3, and H3K27ac) in a series of mouse embryonic stem cells (mESCs) with varying DNA methylation levels to study the effects of DNA methylation on deposition of histone modifications. We find that genome-wide DNA demethylation alters occupancy of histone modifications at both promoters and enhancers. This is reversed upon remethylation by Dnmt expression. DNA methylation promotes H3K27me3 deposition at bivalent promoters, while opposing H3K27me3 at silent promoters. DNA methylation also reversibly regulates H3K27ac and H3K27me3 at previously identified tissue-specific enhancers. These effects require DNMT catalytic activity. Collectively, our data show that DNA methylation is essential and instructive for deposition of specific histone modifications across regulatory regions, which together influences gene expression patterns in mESCs.

Scientific Abstract:

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